



Welcome to the  
**BioInformatics & Molecular Analysis Section (BIMAS)**



## HLA Peptide Binding Predictions

**Function:** Rank potential 8-mer, 9-mer, or 10-mer peptides based on a predicted half-time of dissociation to HLA class I molecules. The analysis is based on coefficient tables deduced from the published literature by Dr. Kenneth Parker [kparker@atlas.niaid.nih.gov](mailto:kparker@atlas.niaid.nih.gov), NIAID, NIH.

Another web site for predicting which peptides bind to MHC molecules is SYFPEITHI, developed by Hans-Georg Rammensee's lab.

**Analysis Options:****HLA molecule****n-mers**

A1
A_0201
A_0205
A24
A3

9
---

**Results Limited by:**  **Explicit Number**  **Predicted T<sub>(%)</sub> >=**

20
----

100
-----

Please enter or paste an AA sequence to analyze (most formats accepted):

Echo input sequence (generally recommended)

*Credits: WWW implementation by Ronald Taylor of BIMAS / CBEL / CIT / NIH*

If you use results from this analysis in published research, please cite:

*Parker, K. C., M. A. Bednarek, and J. E. Coligan. 1994. Scheme for ranking potential HLA-A2 binding peptides based on independent binding of individual peptide side-chains. J. Immunol. 152:163.*



[Return to BIMAS home page](#)



National  
Library  
of Medicine

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
<input type="text" value="Search PubMed"/> <input type="button" value="Go"/> <input type="button" value="Clear"/>					<input type="button" value="Limits"/>	<input type="button" value="Preview/Index"/>	<input type="button" value="History"/>	<input type="button" value="Clipboard"/>
<input type="button" value="Display"/> <input type="button" value="Abstract"/> <input type="button" value="Save"/> <input type="button" value="Text"/> <input type="button" value="Order"/> <input type="button" value="Add to Clipboard"/>								

Entrez PubMed

1: *AIDS Res Hum Retroviruses* 1997 May 1;13(7):529-31      Books, LinkOut

PubMed Services



Related Resources

## An interactive Web site providing major histocompatibility ligand predictions: application to HIV research.

De Groot AS, Jesdale BM, Szu E, Schafer JR, Chicz RM, Deocampo G

TB/HIV Research Laboratory, Brown University School of Medicine,  
Providence, Rhode Island 02912, USA.

EpiMatrix/HIV, a tool that is currently available on the World Wide Web, enables researchers to screen HIV proteins for potential MHC ligands. We have performed a comparison of EpiMatrix predictions to 158 published allotype-specific HLA-associated peptides (MHC ligands) derived from 133 proteins. The top 10 ranked EpiMatrix predictions for each of the 158 HLA allotype-protein pairs were selected for comparison with these published ligands. EpiMatrix correctly identified 134 of 158 published ligands (85%). The algorithm is now available for use by the HIV research community at the URL <http://www.EpiMatrix.com/HIV>.

PMID: 9135870

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Freedom of Information Act](#) | [Disclaimer](#)